

Claims

- Sub C1
1. A method for modifying the carbohydrate composition of a plant or plant organ characterized by the growing of a transgenic plant containing an expression cassette which contains a DNA sequence encoding a (primary) enzyme of interest capable of degrading a plant polysaccharide, under conditions conducive whereby said enzyme-encoding DNA sequence is expressed and the carbohydrate composition of said plant or plant organ is modified, with the proviso that if said plant or plant organ is potato, the DNA sequence encoding said (primary) enzyme of interest originates from a microbial source.
2. The method of claim 1 further characterized in that said expression cassette contains a regulatory sequence capable of directing the expression of said enzyme of interest at a selected maturity stage of the development of the transgenic plant or plant organ.
3. The method of claim 1 further characterized in that said expression construct is capable of directing the tissue-specific expression of said enzyme of interest.
4. The method of claim 1 further characterized in that the DNA sequence encoding said (primary) enzyme of interest is provided with a leader sequence capable of targeting the expressed enzyme to a pre-determined cellular compartment or organelle.
5. The method of claim 1 further characterized in that an increase in the content of soluble saccharides containing up to six monosaccharide units is obtained in said transgenic plant or plant organ as a result of the action of said enzyme of interest.
6. The method of claim 1 wherein said (primary) enzyme of interest is selected from the group selected from amylases, glucanases, cellulases, endoglucanases, arabinanases,

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galactanases, mannanases, xylanases, fucosidases, rhamnosidases, levanase and inulanase.

7. The method of claim 1 wherein the DNA sequence encoding said (primary) enzyme of interest originates from a microbial source.

8. The method of claim 7 wherein the DNA sequence encoding said (primary) enzyme of interest is selected from the group consisting of an α -amylase originating from Bacillus licheniformis and a glucoamylase originating from Aspergillus niger.

9. The method according to claim 1 further characterized in that said transgenic plant contains one or more expression constructs containing DNA constructs encoding a secondary enzyme of interest other than and in addition to said (primary) enzyme of interest, said secondary enzyme of interest being capable of using the starch degradation products resulting from the action of said primary enzyme of interest as a substrate.

10. The method of claim 9 further characterized in that said additional enzyme of interest is selected from the group consisting of glucoamylases, pullulanases, isoamylases, cyclomaltodextrin-D-glucotransferases, α -(1-4)-glucanases, α -(1-4)-glucosidases, α -(1-6)-glucosidases, β -glucosidases, D-glucoseisomerases and inulinases.

11. The method of any one of claims 1 - 10 further characterized in that said transgenic plant is selected from the group consisting of tomato, potato, corn, cassave, carrot, lettuce, strawberry and tobacco.

12. An expression construct characterized in that a DNA sequence encoding an enzyme of interest capable of degrading a plant polysaccharide is operably linked to a regulatory sequence capable of directing the expression of said enzyme of interest at a selected maturity stage of the development

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